SEQUENCE LISTING

<110> Chiorini, John
      Kotin, Robert M.
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      Davidson, Elizabeth
      Zabner, Joseph

<120> AAV5 VECTOR FOR TRANSDUCING BRAIN CELLS AND LUNG CELLS

<130> 14014.0323U2

<140> 09/533,427
<141> 2000-03-22

<160> 26

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 4652
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 1

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caaagagctg ccagacgacg gccctctggc cgtcgccccc ccaaacgagc cagcgagcga    120
gcgaacgcga caggggggag agtgccacac tctcaagcaa gggggttttg taagcagtga    180
tgtcataatg atgtaatgct tattgtcacg cgatagttaa tgattaacag tcatgtgatg    240
tgtttttatcc aataggaaga aagcgcgcgt atgagttctc gcgagacttc cggggtataa    300
aagaccgagt gaacgagccc gccgccattc tttgctctgg actgctagag gaccctcgct    360
gccatggcta ccttctatga agtcattgtt cgcgtcccat ttgacgtgga ggaacatctg    420
cctggaattt ctgacagctt tgtggactgg gtaactggtc aaatttggga gctgcctcca    480
gagtcagatt taaatttgac tctggttgaa cagcctcagt tgacggtggc tgatagaatt    540
cgccgcgtgt tcctgtacga gtggaacaaa ttttccaagc aggagtccaa attctttgtg    600
cagtttgaaa agggatctga atatttcat ctgcacacgc ttgtggagac ctccggcatc    660
tcttccatgg tcctcggccg ctacgtgagt cagattcgcg cccagctggt gaaagtggtc    720
ttccagggaa ttgaacccca gatcaacgac tgggtcgcca tcaccaaggt aaagaagggc    780
ggagccaata aggtggtgga ttctgggtat attcccgcct acctgctgcc gaaggtccaa    840
ccggagcttc agtgggcgtg gacaaacctg gacgagtata aattggccgc cctgaatctg    900
gaggagcgca aacggctcgt cgcgcagttt ctggcagaat cctcgcagcg ctcgcaggag    960
gcggcttcgc agcgtgagtt ctcggctgac ccggtcatca aaagcaagac ttcccagaaa   1020
tacatggcgc tcgtcaactg gctcgtggag cacggcatca cttccgagaa gcagtggatc   1080
caggaaaatc aggagagcta cctctccttc aactccaccg gcaactctcg gagccagatc   1140
aaggccgcgc tcgacaacgc gaccaaaatt atgagtctga caaaaagcgc ggtggactac   1200
ctcgtgggga gctccgttcc cgaggacatt tcaaaaaaca gaatctggca aatttttgag   1260
atgaatggct acgacccggc ctacgcggga tccatcctct acggctggtg tcagcgctcc   1320
ttcaacaaga ggaacaccgt ctggctctac ggacccgcca cgaccggcaa gaccaacatc   1380
gcggaggcca tcgcccacac tgtgccctt tacggctgcg tgaactggac caatgaaaac   1440
tttcccttta tgactgtgt ggacaaaatg ctcatttggt gggaggaggg aaagatgacc   1500
aacaaggtgg ttgaatccgc caaggccatc ctggggggct caaaggtgcg ggtcgatcag   1560
aaatgtaaat cctctgttca aattgattct accctgtca ttgtaacttc caatacaaac   1620
atgtgtgtgg tggtggatgg gaattccacg acctttgaac accagcagcc gctggaggac   1680
cgcatgttca aatttgaact gactaagcgg ctcccgccag attttggcaa gattactaag   1740
caggaagtca aggacttttt tgcttgggca aaggtcaatc aggtgccggt gactcacgag   1800
tttaaagttc ccagggaatt ggcgggaact aaaggggcgg agaaatctct aaaacgccca   1860
```

```
ctgggtgacg tcaccaatac tagctataaa agtctggaga agcgggccag gctctcattt   1920
gttcccgaga cgcctcgcag ttcagacgtg actgttgatc ccgctcctct gcgaccgctc   1980
aattggaatt caaggtatga ttgcaaatgt gactatcatg ctcaatttga caacatttct   2040
aacaaatgtg atgaatgtga atatttgaat cggggcaaaa atggatgtat ctgtcacaat   2100
gtaactcact gtcaaatttg tcatgggatt cccccctggg aaaaggaaaa cttgtcagat   2160
tttgggggatt ttgacgatgc caataaagaa cagtaaataa agcgagtagt catgtctttt   2220
gttgatcacc ctccagattg gttggaagaa gttggtgaag gtcttcgcga gttttgggc   2280
cttgaagcgg gcccaccgaa accaaaaccc aatcagcagc atcaagatca agcccgtggt   2340
cttgtgctgc ctggttataa ctatctcgga cccggaaacg gtctcgatcg aggagagcct   2400
gtcaacaggg cagacgaggt cgcgcgagag cacgacatct cgtacaacga gcagcttgag   2460
gcgggagaca acccctacct caagtacaac cacgcggacg ccgagtttca ggagaagctc   2520
gccgacgaca catccttcgg gggaaacctc ggaaaggcag tctttcaggc caagaaaagg   2580
gttctcgaac ctttttggcct ggttgaagag ggtgctaaga cggcccctac cggaaagcgg   2640
atagacgacc actttccaaa aagaaagaag gctcggaccg aagaggactc caagccttcc   2700
acctcgtcag acgccgaagc tggacccagc ggatcccagc agctgcaaat cccagcccaa   2760
ccagcctcaa gtttgggagc tgatacaatg tctgcgggag gtggcggccc attgggcgac   2820
aataaccaag gtgccgatgg agtgggcaat gcctcgggag attggcattg cgattccacg   2880
tggatggggg acagagtcgt caccaagtcc acccgaacct gggtgctgcc cagctacaac   2940
aaccaccagt accgagagat caaaagcggc tccgtcgacg gaagcaacgc caacgcctac   3000
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ccccgagact ggcaaagact catcaacaac tactggggct tcagaccccg gtccctcaga   3120
gtcaaaatct tcaacattca agtcaaagag gtcacggtgc aggactccac caccaccatc   3180
gccaacaacc tcacctccac cgtccaagtg tttacggacg acgactacca gctgccctac   3240
gtcgtcggca acgggaccga gggatgcctg ccggccttcc ctccgcaggt ctttacgctg   3300
ccgcagtacg gttacgcgac gctgaaccgc gacaacacag aaaatcccac cgagaggagc   3360
agcttcttct gcctagagta ctttcccagc aagatgctga gaacgggcaa caactttgag   3420
tttacctaca ctttgagga ggtgcccttc cactccagct tcgctcccag tcagaacctg   3480
ttcaagctgg ccaacccgct ggtggaccag tacttgtacc gcttcgtgag cacaaataac   3540
actggcggag tccagttcaa caagaacctg ccgggagat acgccaacac ctacaaaaac   3600
tggttcccgg ggcccatggg ccgaacccag ggctggaacc tgggctccgg ggtcaaccgc   3660
gccagtgtca gcgccttcgc cacgaccaat aggatggagc tcgagggcgc gagttaccag   3720
gtgcccccgc agccgaacgg catgaccaac aacctccagg gcagcaacac ctatgccctg   3780
gagaacacta tgatcttcaa cagccagccg gcgaacccgg gcaccaccgc cacgtacctc   3840
gagggcaaca tgctcatcac cagcgagagc gagacgcagc cggtgaaccg cgtggcgtac   3900
aacgtcggcg ggcagatggc caccaacaac cagagctcca ccactgcccc cgcgaccggc   3960
acgtacaacc tccaggaaat cgtgcccggc agcgtgtgga tggagaggga cgtgtacctc   4020
caaggaccca tctgggccaa gatcccagag acgggggcgc actttcaccc ctctccggcc   4080
atgggcggat cggactcaa acacccaccg cccatgatgc tcatcaagaa cacgcctgtg   4140
cccggaaata tcaccagctt ctcggacgtg cccgtcagca gcttcatcac ccagtacagc   4200
accgggcagg tcaccgtgga gatggagtgg gagctcaaga aggaaaactc caagaggtgg   4260
aacccagaga tccagtacac aaacaactac aacgaccccc agtttgtgga ctttgccccg   4320
gacagcaccg gggaatacag aaccaccaga cctatcggaa cccgatacct tacccgaccc   4380
cttttaaccca ttcatgtcgc ataccctcaa taaccgtgt attcgtgtca gtaaaatact   4440
gcctcttgtg gtcattcaat gaataacagc ttacaacatc tacaaacct ccttgcttga   4500
gagtgtggca ctctccccc tgtcgcgttc gctcgctcgc tggctcgttt ggggggggtgg   4560
cagctcaaag agctgccaga cgacggccct ctggccgtcg cccccccaaa cgagccagcg   4620
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```

<210> 2
<211> 390
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 2
 Met Ala Leu Val Asn Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys
 1   5   10   15

```
Gln Trp Ile Gln Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr
            20                  25                  30
Gly Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Thr Lys
            35                  40                  45
Ile Met Ser Leu Thr Lys Ser Ala Val Asp Tyr Leu Val Gly Ser Ser
    50                  55                  60
Val Pro Glu Asp Ile Ser Lys Asn Arg Ile Trp Gln Ile Phe Glu Met
65                  70                  75                  80
Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Ile Leu Tyr Gly Trp Cys
                85                  90                  95
Gln Arg Ser Phe Asn Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala
            100                 105                 110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            115                 120                 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130                 135                 140
Cys Val Asp Lys Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Asn
145                 150                 155                 160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165                 170                 175
Val Asp Gln Lys Cys Lys Ser Ser Val Gln Ile Asp Ser Thr Pro Val
            180                 185                 190
Ile Val Thr Ser Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser
            195                 200                 205
Thr Thr Phe Glu His Gln Gln Pro Leu Glu Asp Arg Met Phe Lys Phe
    210                 215                 220
Glu Leu Thr Lys Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln
225                 230                 235                 240
Glu Val Lys Asp Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val
                245                 250                 255
Thr His Glu Phe Lys Val Pro Arg Glu Leu Ala Gly Thr Lys Gly Ala
            260                 265                 270
Glu Lys Ser Leu Lys Arg Pro Leu Gly Asp Val Thr Asn Thr Ser Tyr
            275                 280                 285
Lys Ser Leu Glu Lys Arg Ala Arg Leu Ser Phe Val Pro Glu Thr Pro
    290                 295                 300
Arg Ser Ser Asp Val Thr Val Asp Pro Ala Pro Leu Arg Pro Leu Asn
305                 310                 315                 320
Trp Asn Ser Arg Tyr Asp Cys Lys Cys Asp Tyr His Ala Gln Phe Asp
                325                 330                 335
Asn Ile Ser Asn Lys Cys Asp Glu Cys Glu Tyr Leu Asn Arg Gly Lys
            340                 345                 350
Asn Gly Cys Ile Cys His Asn Val Thr His Cys Gln Ile Cys His Gly
            355                 360                 365
Ile Pro Pro Trp Glu Lys Glu Asn Leu Ser Asp Phe Gly Asp Phe Asp
    370                 375                 380
Asp Ala Asn Lys Glu Gln
385                 390
```

<210> 3
<211> 610
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

3

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<400> 3
Met Ala Thr Phe Tyr Glu Val Ile Val Arg Val Pro Phe Asp Val Glu
1               5                   10                  15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asp Trp Val Thr Gly
            20                  25                  30
Gln Ile Trp Glu Leu Pro Pro Glu Ser Asp Leu Asn Leu Thr Leu Val
        35                  40                  45
Glu Gln Pro Gln Leu Thr Val Ala Asp Arg Ile Arg Arg Val Phe Leu
    50                  55                  60
Tyr Glu Trp Asn Lys Phe Ser Lys Gln Glu Ser Lys Phe Phe Val Gln
65                  70                  75                  80
Phe Glu Lys Gly Ser Glu Tyr Phe His Leu His Thr Leu Val Glu Thr
                85                  90                  95
Ser Gly Ile Ser Ser Met Val Leu Gly Arg Tyr Val Ser Gln Ile Arg
            100                 105                 110
Ala Gln Leu Val Lys Val Val Phe Gln Gly Ile Glu Pro Gln Ile Asn
            115                 120                 125
Asp Trp Val Ala Ile Thr Lys Val Lys Lys Gly Gly Ala Asn Lys Val
    130                 135                 140
Val Asp Ser Gly Tyr Ile Pro Ala Tyr Leu Leu Pro Lys Val Gln Pro
145                 150                 155                 160
Glu Leu Gln Trp Ala Trp Thr Asn Leu Asp Glu Tyr Lys Leu Ala Ala
                165                 170                 175
Leu Asn Leu Glu Glu Arg Lys Arg Leu Val Ala Gln Phe Leu Ala Glu
            180                 185                 190
Ser Ser Gln Arg Ser Gln Glu Ala Ala Ser Gln Arg Glu Phe Ser Ala
            195                 200                 205
Asp Pro Val Ile Lys Ser Lys Thr Ser Gln Lys Tyr Met Ala Leu Val
    210                 215                 220
Asn Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln
225                 230                 235                 240
Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr Gly Asn Ser Arg
                245                 250                 255
Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Thr Lys Ile Met Ser Leu
            260                 265                 270
Thr Lys Ser Ala Val Asp Tyr Leu Val Gly Ser Ser Val Pro Glu Asp
        275                 280                 285
Ile Ser Lys Asn Arg Ile Trp Gln Ile Phe Glu Met Asn Gly Tyr Asp
    290                 295                 300
Pro Ala Tyr Ala Gly Ser Ile Leu Tyr Gly Trp Cys Gln Arg Ser Phe
305                 310                 315                 320
Asn Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala Thr Thr Gly Lys
                325                 330                 335
Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys
            340                 345                 350
Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys
            355                 360                 365
Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Asn Lys Val Val Glu
    370                 375                 380
Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys
385                 390                 395                 400
Cys Lys Ser Ser Val Gln Ile Asp Ser Thr Pro Val Ile Val Thr Ser
                405                 410                 415
Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser Thr Thr Phe Glu
            420                 425                 430
His Gln Gln Pro Leu Glu Asp Arg Met Phe Lys Phe Glu Leu Thr Lys
            435                 440                 445
Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln Glu Val Lys Asp
    450                 455                 460
Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val Thr His Glu Phe
465                 470                 475                 480
```

4

```
Lys Val Pro Arg Glu Leu Ala Gly Thr Lys Gly Ala Glu Lys Ser Leu
            485             490             495
Lys Arg Pro Leu Gly Asp Val Thr Asn Thr Ser Tyr Lys Ser Leu Glu
        500             505             510
Lys Arg Ala Arg Leu Ser Phe Val Pro Glu Thr Pro Arg Ser Ser Asp
        515             520             525
Val Thr Val Asp Pro Ala Pro Leu Arg Pro Leu Asn Trp Asn Ser Arg
    530             535             540
Tyr Asp Cys Lys Cys Asp Tyr His Ala Gln Phe Asp Asn Ile Ser Asn
545             550             555             560
Lys Cys Asp Glu Cys Glu Tyr Leu Asn Arg Gly Lys Asn Gly Cys Ile
            565             570             575
Cys His Asn Val Thr His Cys Gln Ile Cys His Gly Ile Pro Pro Trp
            580             585             590
Glu Lys Glu Asn Leu Ser Asp Phe Gly Asp Phe Asp Asp Ala Asn Lys
            595             600             605
Glu Gln
    610


<210> 4
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 4
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5               10              15
Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20              25              30
Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35              40              45
Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50              55              60
Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65              70              75              80
Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
            85              90              95
Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
        100             105             110
Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115             120             125
Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130             135             140
Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145             150             155             160
Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
            165             170             175
Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180             185             190
Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
            195             200             205
Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210             215             220
Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225             230             235             240
```

5

```
Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
            245             250             255
Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260             265             270
Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275             280             285
Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290             295             300
Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305             310             315             320
Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
            325             330             335
Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340             345             350
Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
            355             360             365
Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370             375             380
Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385             390             395             400
Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
            405             410             415
Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420             425             430
Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
            435             440             445
Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450             455             460
Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465             470             475             480
Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
            485             490             495
Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500             505             510
Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
            515             520             525
Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
            530             535             540
Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545             550             555             560
Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
            565             570             575
Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580             585             590
Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
            595             600             605
Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610             615             620
Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625             630             635             640
Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
            645             650             655
Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660             665             670
Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
            675             680             685
Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690             695             700
Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705             710             715             720
Thr Arg Pro Leu
```

6

```
<210> 5
<211> 588
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 5
 Thr Ala Pro Thr Gly Lys Arg Ile Asp Asp His Phe Pro Lys Arg Lys
  1               5                  10                  15
 Lys Ala Arg Thr Glu Glu Asp Ser Lys Pro Ser Thr Ser Ser Asp Ala
              20                  25                  30
 Glu Ala Gly Pro Ser Gly Ser Gln Gln Leu Gln Ile Pro Ala Gln Pro
              35                  40                  45
 Ala Ser Ser Leu Gly Ala Asp Thr Met Ser Ala Gly Gly Gly Gly Pro
          50                  55                  60
 Leu Gly Asp Asn Asn Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly
 65                  70                  75                  80
 Asp Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Val Thr Lys
                  85                  90                  95
 Ser Thr Arg Thr Trp Val Leu Pro Ser Tyr Asn Asn His Gln Tyr Arg
              100                 105                 110
 Glu Ile Lys Ser Gly Ser Val Asp Gly Ser Asn Ala Asn Ala Tyr Phe
              115                 120                 125
 Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Ser
              130                 135                 140
 His Trp Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Tyr Trp Gly
 145                 150                 155                 160
 Phe Arg Pro Arg Ser Leu Arg Val Lys Ile Phe Asn Ile Gln Val Lys
                  165                 170                 175
 Glu Val Thr Val Gln Asp Ser Thr Thr Thr Ile Ala Asn Asn Leu Thr
              180                 185                 190
 Ser Thr Val Gln Val Phe Thr Asp Asp Asp Tyr Gln Leu Pro Tyr Val
              195                 200                 205
 Val Gly Asn Gly Thr Glu Gly Cys Leu Pro Ala Phe Pro Pro Gln Val
              210                 215                 220
 Phe Thr Leu Pro Gln Tyr Gly Tyr Ala Thr Leu Asn Arg Asp Asn Thr
 225                 230                 235                 240
 Glu Asn Pro Thr Glu Arg Ser Ser Phe Phe Cys Leu Glu Tyr Phe Pro
                  245                 250                 255
 Ser Lys Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Thr Tyr Asn Phe
              260                 265                 270
 Glu Glu Val Pro Phe His Ser Ser Phe Ala Pro Ser Gln Asn Leu Phe
              275                 280                 285
 Lys Leu Ala Asn Pro Leu Val Asp Gln Tyr Leu Tyr Arg Phe Val Ser
     290                 295                 300
 Thr Asn Asn Thr Gly Gly Val Gln Phe Asn Lys Asn Leu Ala Gly Arg
 305                 310                 315                 320
 Tyr Ala Asn Thr Tyr Lys Asn Trp Phe Pro Gly Pro Met Gly Arg Thr
              325                 330                 335
 Gln Gly Trp Asn Leu Gly Ser Gly Val Asn Arg Ala Ser Val Ser Ala
              340                 345                 350
 Phe Ala Thr Thr Asn Arg Met Glu Leu Glu Gly Ala Ser Tyr Gln Val
              355                 360                 365
 Pro Pro Gln Pro Asn Gly Met Thr Asn Asn Leu Gln Gly Ser Asn Thr
     370                 375                 380
```

7

```
Tyr Ala Leu Glu Asn Thr Met Ile Phe Asn Ser Gln Pro Ala Asn Pro
385                 390                 395                 400
Gly Thr Thr Ala Thr Tyr Leu Glu Gly Asn Met Leu Ile Thr Ser Glu
            405                 410                 415
Ser Glu Thr Gln Pro Val Asn Arg Val Ala Tyr Asn Val Gly Gly Gln
            420                 425                 430
Met Ala Thr Asn Asn Gln Ser Ser Thr Thr Ala Pro Ala Thr Gly Thr
            435                 440                 445
Tyr Asn Leu Gln Glu Ile Val Pro Gly Ser Val Trp Met Glu Arg Asp
    450                 455                 460
Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro Glu Thr Gly Ala
465                 470                 475                 480
His Phe His Pro Ser Pro Ala Met Gly Gly Phe Gly Leu Lys His Pro
            485                 490                 495
Pro Pro Met Met Leu Ile Lys Asn Thr Pro Val Pro Gly Asn Ile Thr
            500                 505                 510
Ser Phe Ser Asp Val Pro Val Ser Ser Phe Ile Thr Gln Tyr Ser Thr
            515                 520                 525
Gly Gln Val Thr Val Glu Met Glu Trp Glu Leu Lys Lys Glu Asn Ser
    530                 535                 540
Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Asn Asn Tyr Asn Asp Pro
545                 550                 555                 560
Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly Glu Tyr Arg Thr Thr
            565                 570                 575
Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
            580                 585
```

<210> 6
<211> 532
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 6

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Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
1               5               10              15
Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
            20              25              30
Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
        35              40              45
Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
    50              55              60
Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
65              70              75              80
Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
            85              90              95
Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
            100             105             110
Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
        115             120             125
Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
    130             135             140
Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
145             150             155             160
Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
            165             170             175
Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
            180             185             190
```

```
Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
        195                 200                 205
Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
    210                 215                 220
Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
225                 230                 235                 240
Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
                245                 250                 255
Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
            260                 265                 270
Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
            275                 280                 285
Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
    290                 295                 300
Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
305                 310                 315                 320
Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
                325                 330                 335
Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
            340                 345                 350
Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
            355                 360                 365
Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
    370                 375                 380
Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
385                 390                 395                 400
Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
                405                 410                 415
Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
            420                 425                 430
Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
            435                 440                 445
Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
    450                 455                 460
Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
465                 470                 475                 480
Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
                485                 490                 495
Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
            500                 505                 510
Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
            515                 520                 525
Thr Arg Pro Leu
    530
```

<210> 7
<211> 2307
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

```
      <400> 7
aggctctcat ttgttcccga dacgcctcgc agttcagacg tgactgttga tcccgctcct      60
ctgcgaccgc tcaattggaa ttcaagtaaa taaagcgagt agtcatgtct tttgttgatc     120
accctccaga ttggttggaa gaagttggtg aaggtcttcg cgagttttg ggccttgaag      180
cgggcccacc gaaaccaaaa cccaatcagc agcatcaaga tcaagcccgt ggtcttgtgc     240
tgcctggtta taactatctc ggacccggaa acggtctcga tcgaggagag cctgtcaaca     300
gggcagacga ggtcgcgcga gagcacgaca tctcgtacaa cgagcagctt gaggcgggag     360
```

9

```
acaacccta cctcaagtac aaccacgcgg acgccgagtt tcaggagaag ctcgccgacg    420
acacatcctt cgggggaaac ctcggaaagg cagtctttca ggccaagaaa agggttctcg    480
aacctttgg cctggttgaa gagggtgcta agacggcccc taccggaaag cggatagacg    540
accactttcc aaaaagaaag aaggctcgga ccgaagagga ctccaagcct tccacctcgt    600
cagacgccga agctggaccc agcggatccc agcagctgca aatcccagcc caaccagcct    660
caagtttggg agctgataca atgtctgcgg gaggtggcgg cccattgggc gacaataacc    720
aaggtgccga tggagtgggc aatgcctcgg gagattggca ttgcgattcc acgtggatgg    780
gggacagagt cgtcaccaag tccacccgaa cctgggtgct gcccagctac aacaaccacc    840
agtaccgaga gatcaaaagc ggctccgtcg acggaagcaa cgccaacgcc tactttggat    900
acagcacccc ctggggggtac tttgacttta accgcttcca cagccactgg agcccccgag    960
actggcaaag actcatcaac aactactggg gcttcagacc ccggtccctc agagtcaaaa   1020
tcttcaacat tcaagtcaaa gaggtcacgg tgcaggactc caccaccacc atcgccaaca   1080
acctcacctc caccgtccaa gtgtttacgg acgacgacta ccagctgccc tacgtcgtcg   1140
gcaacgggac cgagggatgc ctgccggcct tccctccgca ggtctttacg ctgccgcagt   1200
acggttacgc gacgctgaac cgcgacaaca cagaaaatcc caccgagagg agcagcttct   1260
tctgcctaga gtactttccc agcaagatgc tgagaacggg caacaacttt gagtttacct   1320
acaactttga ggaggtgccc ttccactcca gcttcgctcc cagtcagaac ctgttcaagc   1380
tggccaaccc gctggtggac cagtacttgt accgcttcgt gagcacaaat aacactggcg   1440
gagtccagtt caacaagaac ctggccggga gatacgccaa cacctacaaa aactggttcc   1500
cggggcccat gggccgaacc cagggctgga acctgggctc cggggtcaac cgcgccagtg   1560
tcagcgcctt cgccacgacc aataggatgg agctcgaggg cgcgagttac caggtgcccc   1620
cgcagccgaa cggcatgacc aacaacctcc agggcagcaa cacctatgcc ctggagaaca   1680
ctatgatctt caacagccag ccggcgaacc cgggcaccac cgccacgtac ctcgagggca   1740
acatgctcat caccagcgag agcgagacgc agccggtgaa ccgcgtggcg tacaacgtcg   1800
gcgggcagat ggccaccaac aaccagagct ccaccactgc ccccgcgacc ggcacgtaca   1860
acctccagga aatcgtgccc ggcagcgtgt ggatggagag ggacgtgtac ctccaaggac   1920
ccatctgggc caagatccca gagacggggg cgcactttca cccctctccg gccatgggcg   1980
gattcggact caaacaccca ccgcccatga tgctcatcaa gaacacgcct gtgcccggaa   2040
atatcaccag cttctcggac gtgcccgtca gcagcttcat cacccagtac agcaccgggc   2100
aggtcaccgt ggagatggag tgggagctca agaaggaaaa ctccaagagg tggaacccag   2160
agatccagta cacaaacaac tacaacgacc cccagtttgt ggactttgcc ccggacagca   2220
ccggggaata cagaaccacc agacctatcg gaacccgata ccttacccga cccctttaac   2280
ccattcatgt cgcataccct caataaa                                       2307
```

<210> 8
<211> 2264
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 8

```
aggctctcat ttgttcccga gacgcctcgc agttcagacg tgactgttga tcccgctcct     60
ctgcgaccgc tcaattggaa ttcaagattg gttggaagaa gttggtgaag gtcttcgcga    120
gttttgggc cttgaagcgg gcccaccgaa accaaaaccc aatcagcagc atcaagatca    180
agcccgtggt cttgtgctgc ctggttataa ctatctcgga cccggaaacg gtctcgatcg    240
aggagagcct gtcaacaggg cagacgaggt cgcgcgagag cacgacatct cgtacaacga    300
gcagcttgag gcgggagaca accctacct caagtacaac cacgcggacg ccgagtttca    360
ggagaagctc gccgacgaca tccttcggg gaaacctc ggaaaggcag tctttcaggc    420
caagaaaagg gttctcgaac cttttggcct ggttgaagag ggtgctaaga cggccctac    480
cggaaagcgg atagacgacc actttccaaa aagaaagaag gctcggaccg aagaggactc    540
caagccttcc acctcgtcag acgccgaagc tggacccagc ggatcccagc agctgcaaat    600
cccagcccaa ccagcctcaa gtttgggagc tgatacaatg tctgcgggag gtggcggccc    660
attgggcgac aataaccaag gtgccgatgg agtgggcaat gcctcgggag attggcattg    720
cgattccacg tggatggggg acagagtcgt caccaagtcc acccgaacct gggtgctgcc    780
cagctacaac aaccaccagt accgagagat caaaagcggc tccgtcgacg gaagcaacgc    840
caacgcctac tttggataca gcacccctg ggggtacttt gactttaacc gcttccacag    900
ccactggagc ccccgagact ggcaaagact catcaacaac tactggggct tcagaccccg    960
gtccctcaga gtcaaaatct tcaacattca agtcaaagag gtcacggtgc aggactccac   1020
```

```
caccaccatc gccaacaacc tcacctccac cgtccaagtg tttacggacg acgactacca      1080
gctgccctac gtcgtcggca acgggaccga gggatgcctg ccggccttcc ctccgcaggt      1140
ctttacgctg ccgcagtacg gttacgcgac gctgaaccgc gacaacacag aaaatcccac      1200
cgagaggagc agcttcttct gcctagagta ctttcccagc aagatgctga gaacgggcaa      1260
caactttgag tttacctaca actttgagga ggtgcccttc cactccagct tcgctcccag      1320
tcagaacctg ttcaagctgg ccaacccgct ggtggaccag tacttgtacc gcttcgtgag      1380
cacaaataac actggcggag tccagttcaa caagaacctg gccgggagat acgccaacac      1440
ctacaaaaac tggttcccgg ggcccatggg ccgaacccag ggctggaacc tgggctccgg      1500
ggtcaaccgc gccagtgtca gcgccttcgc cacgaccaat aggatggagc tcgagggcgc      1560
gagttaccag gtgcccccgc agccgaacgg catgaccaac aacctccagg gcagcaacac      1620
ctatgccctg gagaacacta tgatcttcaa cagccagccg gcgaacccgg gcaccaccgc      1680
cacgtacctc gagggcaaca tgctcatcac cagcgagagc gagacgcagc cggtgaaccg      1740
cgtggcgtac aacgtcggcg ggcagatggc caccaacaac cagagctcca ccactgcccc      1800
cgcgaccggc acgtacaacc tccaggaaat cgtgcccggc agcgtgtgga tggagaggga      1860
cgtgtacctc caaggaccca tctgggccaa gatcccagag acggggcgc actttcaccc      1920
ctctccggcc atgggcggat tcggactcaa acacccaccg cccatgatgc tcatcaagaa      1980
cacgcctgtg cccggaaata tcaccagctt ctcggacgtg cccgtcagca gcttcatcac      2040
ccagtacagc accgggcagg tcaccgtgga gatggagtgg gagctcaaga aggaaaactc      2100
caagaggtgg aacccagaga tccagtacac aaacaactac aacgacccc agtttgtgga      2160
ctttgccccg gacagcaccg gggaatacag aaccaccaga cctatcggaa cccgatacct      2220
tacccgaccc ctttaaccca ttcatgtcgc ataccctcaa taaa                      2264
```

<210> 9
<211> 2264
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 9

```
aggctctcat ttgttcccga gacgcctcgc agttcagacg tgactgttga tcccgctcct        60
ctgcgaccgc tcaattggaa ttcaagattg gttggaagaa gttggtgaag gtcttcgcga       120
gtttttgggc cttgaagcgg gcccaccgaa accaaaaccc aatcagcagc atcaagatca       180
agcccgtggt cttgtgctgc ctggttataa ctatctcgga cccggaaacg gtctcgatcg       240
aggagagcct gtcaacaggg cagacgaggt cgcgcgagag cacgacatct cgtacaacga       300
gcagcttgag gcgggagaca accccacctt caagtacaac cacgcggacg ccgagtttca       360
ggagaagctc gccgacgaca catccttcgg gggaaacctc ggaaaggcag tctttcaggc       420
caagaaaagg gttctcgaac cttttggcct ggttgaagag ggtgctaaga cggcccctac       480
cggaaagcgg atagacgacc actttccaaa aagaaagaag gctcggaccg aagaggactc       540
caagccttcc acctcgtcag acgccgaagc tggacccagc ggatcccagc agctgcaaat       600
cccagcccaa ccagcctcaa gtttgggagc tgatacaatg tctgcgggag gtggcggccc       660
attgggcgac aataaccaag gtgccgatgg agtgggcaat gcctcgggag attggcattg       720
cgattccacg tggatggggg acagagtcgt caccaagtcc acccgaacct gggtgctgcc       780
cagctacaac aaccaccagt accgagagat caaaagcggc tccgtcgacg gaagcaacgc       840
caacgcctac tttggataca gcaccccctg ggggtacttt gactttaacc gcttccacag       900
ccactggagc ccccgagact ggcaaagact catcaacaac tactggggct tcagaccccg       960
gtccctcaga gtcaaaatct tcaacattca agtcaaagag gtcacggtgc aggactccac      1020
caccaccatc gccaacaacc tcacctccac cgtccaagtg tttacggacg acgactacca      1080
gctgccctac gtcgtcggca acgggaccga gggatgcctg ccggccttcc ctccgcaggt      1140
ctttacgctg ccgcagtacg gttacgcgac gctgaaccgc gacaacacag aaaatcccac      1200
cgagaggagc agcttcttct gcctagagta ctttcccagc aagatgctga gaacgggcaa      1260
caactttgag tttacctaca actttgagga ggtgcccttc cactccagct tcgctcccag      1320
tcagaacctg ttcaagctgg ccaacccgct ggtggaccag tacttgtacc gcttcgtgag      1380
cacaaataac actggcggag tccagttcaa caagaacctg gccgggagat acgccaacac      1440
ctacaaaaac tggttcccgg ggcccatggg ccgaacccag ggctggaacc tgggctccgg      1500
ggtcaaccgc gccagtgtca gcgccttcgc cacgaccaat aggatggagc tcgagggcgc      1560
gagttaccag gtgcccccgc agccgaacgg catgaccaac aacctccagg gcagcaacac      1620
ctatgccctg gagaacacta tgatcttcaa cagccagccg gcgaacccgg gcaccaccgc      1680
cacgtacctc gagggcaaca tgctcatcac cagcgagagc gagacgcagc cggtgaaccg      1740
```

```
cgtggcgtac aacgtcggcg ggcagatggc caccaacaac cagagctcca ccactgcccc    1800
cgcgaccggc acgtacaacc tccaggaaat cgtgcccggc agcgtgtgga tggagaggga    1860
cgtgtacctc caaggaccca tctgggccaa gatcccagag acggggggcgc actttcaccc   1920
ctctccggcc atgggcggat tcggactcaa acacccaccg cccatgatgc tcatcaagaa    1980
cacgcctgtg cccggaaata tcaccagctt ctcggacgtg cccgtcagca gcttcatcac    2040
ccagtacagc accgggcagg tcaccgtgga gatggagtgg gagctcaaga aggaaaactc    2100
caagaggtgg aacccagaga tccagtacac aaacaactac aacgaccccc agtttgtgga    2160
ctttgccccg gacagcaccg gggaatacag aaccaccaga cctatcggaa cccgataccc    2220
tacccgaccc ctttaaccca ttcatgtcgc ataccctcaa taaa                     2264
```

<210> 10
<211> 1292
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 10

```
agcgcaaacg gctcgtcgcg cagtttctgg cagaatcctc gcagcgctcg caggaggcgg     60
cttcgcagcg tgagttctcg gctgacccgg tcatcaaaag caagacttcc cagaaataca    120
tggcgctcgt caactggctc gtggagcacg gcatcacttc cgagaagcag tggatccagg    180
aaaatcagga gagctacctc tccttcaact ccaccggcaa ctctcggagc cagatcaagg    240
ccgcgctcga caacgcgacc aaaattatga gtctgacaaa aagcgcggtg gactacctcg    300
tggggagctc cgttcccgag gacatttcaa aaaacagaat ctggcaaatt tttgagatga    360
atggctacga cccggcctac gcgggatcca tcctctacgg ctggtgtcag cgctccttca    420
acaagaggaa caccgtctgg ctctacggac ccgccacgac cggcaagacc aacatcgcgg    480
aggccatcgc ccacactgtg ccctttttacg gctgcgtgaa ctggaccaat gaaaactttc    540
cctttaatga ctgtgtggac aaaatgctca tttggtggga ggagggaaag atgaccaaca    600
aggtggttga atccgccaag gccatcctgg ggggctcaaa ggtgcgggtc gatcagaaat    660
gtaaatcctc tgttcaaatt gattctaccc ctgtcattgt aacttccaat acaaacatgt    720
gtgtggtggt ggatgggaat tccacgacct ttgaacacca gcagccgctg gaggaccgca    780
tgttcaaatt tgaactgact aagcggctcc cgccagattt tggcaagatt actaagcagg    840
aagtcaagga cttttttgct tgggcaaagg tcaatcaggt gccggtgact cacgagttta    900
aagttcccag ggaattggcg ggaactaaag gggcggagaa atctctaaaa cgcccactgg    960
gtgacgtcac caatactagc tataaaagtc tggagaagcg ggccaggctc tcatttgttc   1020
ccgagacgcc tcgcagttca gacgtgactg ttgatcccgc tcctctgcga ccgctcaatt   1080
ggaattcaag gtatgattgc aaatgtgact atcatgctca atttgacaac atttctaaca   1140
aatgtgatga atgtgaatat ttgaatcggg gcaaaaatgg atgtatctgt cacaatgtaa   1200
ctcactgtca aatttgtcat gggattcccc cctgggaaaa ggaaaacttg tcagattttg   1260
gggattttga cgatgccaat aaagaacagt aa                                 1292
```

<210> 11
<211> 1870
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 11

```
attctttgct ctggactgct agaggaccct cgctgccatg gctaccttct atgaagtcat     60
tgttcgcgtc ccatttgacg tggaggaaca tctgcctgga atttctgaca gctttgtgga    120
ctgggtaact ggtcaaattt gggagctgcc tccagagtca gatttaaatt tgactctggt    180
tgaacagcct cagttgacgg tggctgatag aattcgccgc gtgttcctgt acgagtggaa    240
caaattttcc aagcaggagt ccaaattctt tgtgcagttt gaaaagggat ctgaatattt    300
tcatctgcac acgcttgtgg agacctccgg catctcttcc atggtcctcg ccgctacgt     360
gagtcagatt cgcgcccagc tggtgaaagt ggtcttccag ggaattgaac cccagatcaa    420
```

```
cgactgggtc gccatcacca aggtaaagaa gggcggagcc aataaggtgg tggattctgg    480
gtatattccc gcctacctgc tgccgaaggt ccaaccggag cttcagtggg cgtggacaaa    540
cctggacgag tataaattgg ccgccctgaa tctggaggag cgcaaacggc tcgtcgcgca    600
gtttctggca gaatcctcgc agcgctcgca ggaggcggct tcgcagcgtg agttctcggc    660
tgacccggtc atcaaaagca agacttccca gaaatacatg gcgctcgtca actggctcgt    720
ggagcacggc atcacttccg agaagcagtg gatccaggaa aatcaggaga gctacctctc    780
cttcaactcc accggcaact ctcggagcca gatcaaggcc gcgctcgaca acgcgaccaa    840
aattatgagt ctgacaaaaa gcgcggtgga ctacctcgtg gggagctccg ttcccgagga    900
catttcaaaa aacagaatct ggcaaatttt tgagatgaat ggctacgacc cggcctacgc    960
gggatccatc ctctacggct ggtgtcagcg ctccttcaac aagaggaaca ccgtctggct   1020
ctacggaccc gccacgaccg gcaagaccaa catcgcggag gccatcgccc acactgtgcc   1080
cttttacggc tgcgtgaact ggaccaatga aaactttccc tttaatgact gtgtggacaa   1140
aatgctcatt tggtgggagg agggaaagat gaccaacaag gtggttgaat ccgccaaggc   1200
catcctgggg ggctcaaagg tgcgggtcga tcagaaatgt aaatcctctg ttcaaattga   1260
ttctaccccct gtcattgtaa cttccaatac aaacatgtgt gtggtggtgg atgggaattc   1320
cacgaccttt gaacaccagc agccgctgga ggaccgcatg ttcaaatttg aactgactaa   1380
gcggctcccg ccagattttg gcaagattac taagcaggaa gtcaaggact ttttttgcttg   1440
ggcaaaggtc aatcaggtgc cggtgactca cgagtttaaa gttcccaggg aattggcggg   1500
aactaaaggg gcggagaaat ctctaaaacg cccactgggt gacgtcacca atactagcta   1560
taaaagtctg gagaagcggg ccaggctctc atttgttccc gagacgcctc gcagttcaga   1620
cgtgactgtt gatcccgctc ctctgcgacc gctcaattgg aattcaaggt atgattgcaa   1680
atgtgactat catgctcaat ttgacaacat ttctaacaaa tgtgatgaat gtgaatattt   1740
gaatcggggc aaaaatggat gtatctgtca caatgtaact cactgtcaaa tttgtcatgg   1800
gattccccccc tgggaaaagg aaaacttgtc agattttggg gattttgacg atgccaataa   1860
agaacagtaa                                                          1870
```

<210> 12
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
    synthetic construct

<400> 12

```
Met Ala Leu Val Asn Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys
 1               5                  10                  15
Gln Trp Ile Gln Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr
            20                  25                  30

Gly Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Thr Lys
        35                  40                  45
Ile Met Ser Leu Thr Lys Ser Ala Val Asp Tyr Leu Val Gly Ser Ser
    50                  55                  60
Val Pro Glu Asp Ile Ser Lys Asn Arg Ile Trp Gln Ile Phe Glu Met
65                  70                  75                  80
Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Ile Leu Tyr Gly Trp Cys
                85                  90                  95
Gln Arg Ser Phe Asn Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala
            100                 105                 110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115                 120                 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        130                 135                 140
Cys Val Asp Lys Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Asn
145                 150                 155                 160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165                 170                 175
Val Asp Gln Lys Cys Lys Ser Ser Val Gln Ile Asp Ser Thr Pro Val
            180                 185                 190
```

13

```
Ile Val Thr Ser Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser
        195             200                 205
Thr Thr Phe Glu His Gln Gln Pro Leu Glu Asp Arg Met Phe Lys Phe
        210             215                 220
Glu Leu Thr Lys Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln
225             230                 235                 240
Glu Val Lys Asp Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val
            245                 250                 255
Thr His Glu Phe Lys Val Pro Arg Glu Leu Ala Gly Thr Lys Gly Ala
                260                 265                 270
Glu Lys Ser Leu Lys Arg Pro Leu Gly Asp Val Thr Asn Thr Ser Tyr
        275             280                 285
Lys Ser Leu Glu Lys Arg Ala Arg Leu Ser Phe Val Pro Glu Thr Pro
    290             295                 300
Arg Ser Ser Asp Val Thr Val Asp Pro Ala Pro Leu Arg Pro Leu Asn
305             310                 315                 320
Trp Asn Ser Arg Leu Val Gly Arg Ser Trp
            325             330
```

<210> 13
<211> 1115
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 13
```
aggagcgcaa acggctcgtc gcgcagtttc tggcagaatc ctcgcagcgc tcgcaggagg     60
cggcttcgca gcgtgagttc tcggctgacc cggtcatcaa aagcaagact tcccagaaat    120
acatggcgct cgtcaactgg ctcgtggagc acggcatcac ttccgagaag cagtggatcc    180
aggaaaatca ggagagctac ctctccttca actccaccgg caactctcgg agccagatca    240
aggccgcgct cgacaacgcg accaaaatta tgagtctgac aaaaagcgcg gtggactacc    300
tcgtggggag ctccgttccc gaggacattt caaaaaacag aatctggcaa attttttgaga    360
tgaatggcta cgacccggcc tacgcgggat ccatcctcta cggctggtgt cagcgctcct    420
tcaacaagag gaacaccgtc tggctctacg gacccgccac gaccggcaag accaacatcg    480
cggaggccat cgcccacact gtgccctttt acggctgcgt gaactggacc aatgaaaact    540
ttcccttttaa tgactgtgtg gacaaaatgc tcatttggtg ggaggaggga aagatgacca    600
acaaggtggt tgaatccgcc aaggccatcc tggggggctc aaaggtgcgg gtcgatcaga    660
aatgtaaatc ctctgttcaa attgattcta cccctgtcat tgtaacttcc aatacaaaca    720
tgtgtgtggt ggtggatggg aattccacga cctttgaaca ccagcagccg ctggaggacc    780
gcatgttcaa atttgaactg actaagcggc tcccgccaga ttttggcaag attactaagc    840
aggaagtcaa ggactttttt gcttgggcaa aggtcaatca ggtgccggtg actcacgagt    900
ttaaagttcc cagggaattg gcgggaacta aaggggcgga gaaatctcta aaacgcccac    960
tgggtgacgt caccaatact agctataaaa gtctggagaa gcgggccagg ctctcatttg   1020
ttcccgagac gcctcgcagt tcagacgtga ctgttgatcc cgctcctctg cgaccgctca   1080
attggaattc aagattggtt ggaagaagtt ggtga                              1115
```

<210> 14
<211> 550
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 14
```
Met Ala Thr Phe Tyr Glu Val Ile Val Arg Val Pro Phe Asp Val Glu
1               5                   10                  15
```

```
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asp Trp Val Thr Gly
             20              25                  30
Gln Ile Trp Glu Leu Pro Pro Glu Ser Asp Leu Asn Leu Thr Leu Val
         35              40                  45
Glu Gln Pro Gln Leu Thr Val Ala Asp Arg Ile Arg Arg Val Phe Leu
     50              55                  60
Tyr Glu Trp Asn Lys Phe Ser Lys Gln Glu Ser Lys Phe Phe Val Gln
65              70                  75                          80
Phe Glu Lys Gly Ser Glu Tyr Phe His Leu His Thr Leu Val Glu Thr
             85              90                  95
Ser Gly Ile Ser Ser Met Val Leu Gly Arg Tyr Val Ser Gln Ile Arg
             100             105                 110
Ala Gln Leu Val Lys Val Val Phe Gln Gly Ile Glu Pro Gln Ile Asn
         115             120                 125
Asp Trp Val Ala Ile Thr Lys Val Lys Lys Gly Gly Ala Asn Lys Val
     130             135                 140
Val Asp Ser Gly Tyr Ile Pro Ala Tyr Leu Leu Pro Lys Val Gln Pro
145             150             155                         160
Glu Leu Gln Trp Ala Trp Thr Asn Leu Asp Glu Tyr Lys Leu Ala Ala
             165             170                 175
Leu Asn Leu Glu Glu Arg Lys Arg Leu Val Ala Gln Phe Leu Ala Glu
             180             185                 190
Ser Ser Gln Arg Ser Gln Glu Ala Ala Ser Gln Arg Glu Phe Ser Ala
             195             200                 205
Asp Pro Val Ile Lys Ser Lys Thr Ser Gln Lys Tyr Met Ala Leu Val
     210             215                 220
Asn Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln
225             230                 235                     240
Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr Gly Asn Ser Arg
             245             250                 255

Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Thr Lys Ile Met Ser Leu
             260             265                 270
Thr Lys Ser Ala Val Asp Tyr Leu Val Gly Ser Ser Val Pro Glu Asp
         275             280                 285
Ile Ser Lys Asn Arg Ile Trp Gln Ile Phe Glu Met Asn Gly Tyr Asp
     290             295                 300
Pro Ala Tyr Ala Gly Ser Ile Leu Tyr Gly Trp Cys Gln Arg Ser Phe
305             310                 315                     320
Asn Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala Thr Thr Gly Lys
             325                 330                 335
Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys
             340                 345             350
Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys
         355                 360                 365
Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Asn Lys Val Val Glu
370                 375                 380
Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys
385                 390                 395                 400
Cys Lys Ser Ser Val Gln Ile Asp Ser Thr Pro Val Ile Val Thr Ser
             405                 410                 415
Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser Thr Thr Phe Glu
             420                 425                 430
His Gln Gln Pro Leu Glu Asp Arg Met Phe Lys Phe Glu Leu Thr Lys
             435                 440                 445
Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln Glu Val Lys Asp
     450                 455                 460
Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val Thr His Glu Phe
465                 470                 475                 480
Lys Val Pro Arg Glu Leu Ala Gly Thr Lys Gly Ala Glu Lys Ser Leu
             485                 490                 495
```

15

```
Lys Arg Pro Leu Gly Asp Val Thr Asn Thr Ser Tyr Lys Ser Leu Glu
        500                     505                 510
Lys Arg Ala Arg Leu Ser Phe Val Pro Glu Thr Pro Arg Ser Ser Asp
        515                     520                 525
Val Thr Val Asp Pro Ala Pro Leu Arg Pro Leu Asn Trp Asn Ser Arg
        530                     535                 540
Leu Val Gly Arg Ser Trp
545                 550
```

```
<210> 15
<211> 1690
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 15
 attctttgct ctggactgct agaggaccct cgctgccatg gctaccttct atgaagtcat     60
 tgttcgcgtc ccatttgacg tggaggaaca tctgcctgga atttctgaca gctttgtgga    120
 ctgggtaact ggtcaaattt gggagctgcc tccagagtca gatttaaatt tgactctggt    180
 tgaacagcct cagttgacgg tggctgatag aattcgccgc gtgttcctgt acgagtggaa    240
 caaattttcc aagcaggagt ccaaattctt tgtgcagttt gaaaagggat ctgaatattt    300
 tcatctgcac acgcttgtgg agacctccgg catctcttcc atggtcctcg gccgctacgt    360
 gagtcagatt cgcgcccagc tggtgaaagt ggtcttccag ggaattgaac cccagatcaa    420
 cgactgggtc gccatcacca aggtaaagaa gggcggagcc aataaggtgg tggattctgg    480
 gtatattccc gcctacctgc tgccgaaggt ccaaccggag cttcagtggg cgtggacaaa    540
 cctggacgag tataaattgg ccgccctgaa tctggaggag cgcaaacggc tcgtcgcgca    600
 gtttctggca gaatcctcgc agcgctcgca ggaggcggct tcgcagcgtg agttctcggc    660
 tgacccggtc atcaaaagca agacttccca gaaatacatg gcgctcgtca actggctcgt    720
 ggagcacggc atcacttccg agaagcagtg gatccaggaa aatcaggaga gctacctctc    780
 cttcaactcc accggcaact ctcggagcca gatcaaggcc gcgctcgaca cgcgaccaa     840
 aattatgagt ctgacaaaaa gcgcggtgga ctacctcgtg gggagctccg ttcccgagga    900
 catttcaaaa aacagaatct ggcaaatttt tgagatgaat ggctacgacc cggcctacgc    960
 gggatccatc ctctacggct ggtgtcagcg ctccttcaac aagaggaaca ccgtctggct   1020
 ctacggaccc gccacgaccg gcaagaccaa catcgcggag gccatcgccc acactgtgcc   1080
 cttttacggc tgcgtgaact ggaccaatga aaactttccc tttaatgact gtgtggacaa   1140
 aatgctcatt tggtgggagg agggaaagat gaccaacaag gtggttgaat ccgccaaggc   1200
 catcctgggg ggctcaaagg tgcgggtcga tcagaaatgt aaatcctctg ttcaaattga   1260
 ttctacccct gtcattgtaa cttccaatac aaacatgtgt gtggtggtgg atgggaattc   1320
 cacgaccttt gaacaccagc agccgctgga ggaccgcatg ttcaaatttg aactgactaa   1380
 gcggctcccg ccagattttg gcaagattac taagcaggaa gtcaaggact ttttgcttg    1440
 ggcaaaggtc aatcaggtgc cggtgactca cgagtttaaa gttcccaggg aattggcggg   1500
 aactaaaggg gcggagaaat ctctaaaacg cccactgggt gacgtcacca atactagcta   1560
 taaaagtctg gagaagcggg ccaggctctc atttgttccc gagacgcctc gcagttcaga   1620
 cgtgactgtt gatcccgctc tctgcgacc gctcaattgg aattcaagat tggttggaag   1680
 aagttggtga                                                          1690
```

```
<210> 16
<211> 145
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 16
 ccatcaccaa ggtaaagaag ggcggagcca ataaggtggt ggattctggg tatattcccg     60
 cctacctgct gccgaaggtc aaccggagc ttcagtgggc gtggacaaac ctggacgagt    120
```

16

```
  ataaattggc cgccctgaat ctgga                                145
```

<210> 17
<211> 174
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 17
```
  taagcaggaa gtcaaggact tttttgcttg ggcaaaggtc aatcaggtgc cggtgactca     60
  cgagtttaaa gttcccaggg aattggcggg aactaaaggg gcggagaaat ctctaaaacg    120
  cccactgggt gacgtcacca atactagcta taaaagtctg gagaagcggg ccag          174
```

<210> 18
<211> 187
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 18
```
  cactctcaag caaggggggtt ttgtaagcag tgatgtcata atgatgtaat gcttattgtc     60
  acgcgatagt taatgattaa cagtcatgtg atgtgtttta tccaatagga agaaagcgcg    120
  cgtatgagtt ctcgcgagac ttccggggta taaaagaccg agtgaacgag cccgccgcca    180
  ttctttg                                                             187
```

<210> 19
<211> 168
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 19
```
  aaacctcctt gcttgagagt gtggcactct cccccctgtc gcgttcgctc gctcgctggc     60
  tcgtttgggg gggtggcagc tcaaagagct gccagacgac ggccctctgg ccgtcgcccc    120
  cccaaacgag ccagcgagcg agcgaacgcg acaggggga gagtgcca                 168
```

<210> 20
<211> 168
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 20
```
  aaacctcctt gcttgagagt gtggcactct cccccctgtc gcgttcgctc gctcgctggc     60
  tcgtttgggg gggcgacggc cagagggccg tcgtctgccg gctctttgag ctgccacccc    120
  cccaaacgag ccagcgagcg agcgaacgcg acaggggga gagtgcca                 168
```

<210> 21
<211> 8

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 21
 cggtgtga   8

<210> 22
<211> 8
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 22
 cggttgag   8

<210> 23
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 23
 caaaacctcc ttgcttgaga g   21

<210> 24
<211> 4675
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 24
ttggccactc cctctctgcg cgctcgctcg ctcactgagg ccgggcgacc aaaggtcgcc   60
cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag agagggagtg   120
gccaactcca tcactagggg ttcctggagg ggtggagtcg tgacgtgaat tacgtcatag   180
ggttagggag gtcctgtatt agaggtcacg tgagtgtttt gcgacatttt gcgacaccat   240
gtggtcacgc tgggtattta agcccgagtg agcacgcagg gtctccattt tgaagcggga   300
ggtttgaacg cgcagccgcc atgccggggt tttacgagat tgtgattaag gtccccagcg   360
accttgacgg gcatctgccc ggcatttctg acagctttgt gaactgggtg gccgagaagg   420
aatgggagtt gccgccagat tctgacatgg atctgaatct gattgagcag gcacccctga   480
ccgtggccga gaagctgcag cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc   540
cggaggccct tttctttgtg caatttgaga agggagagag ctacttccac atgcacgtgc   600
tcgtggaaac caccgggggt aaatccatgg ttttgggacg tttcctgagt cagattcgcg   660
aaaaactgat tcagagaatt taccgcggga tcgagccgac tttgccaaac tggttcgcgg   720
tcacaaagac cagaaatggc gccggaggcg ggaacaaggt ggtggatgag tgctacatcc   780
ccaattactt gctccccaaa acccagcctg agctccagtg ggcgtggact aatatggaac   840
agtatttaag cgcctgtttg aatctcacgg agcgtaaacg gttggtggcg cagcatctga   900
cgcacgtgtc gcagacgcag gagcagaaca aagagaatca gaatcccaat tctgatgcgc   960

```
cggtgatcag atcaaaaact tcagccaggt acatggagct ggtcgggtgg ctcgtggaca    1020
aggggattac ctcggagaag cagtggatcc aggaggacca ggcctcatac atctccttca    1080
atgcggcctc caactcgcgg tcccaaatca aggctgcctt ggacaatgcg ggaaagatta    1140
tgagcctgac taaaaccgcc cccgactacc tggtgggcca gcagcccgtg gaggacattt    1200
ccagcaatcg gatttataaa attttggaac taaacgggta cgatccccaa tatgcggctt    1260
ccgtctttct gggatgggcc acgaaaaagt tcggcaagag gaacaccatc tggctgtttg    1320
ggcctgcaac taccgggaag accaacatcg cggaggccat agcccacact gtgcccttct    1380
acgggtgcgt aaactggacc aatgagaact ttcccttcaa cgactgtgtc gacaagatgg    1440
tgatctggtg ggaggagggg aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc    1500
tcggaggaag caaggtgcgc gtggaccaga aatgcaagtc ctcggcccag atagacccga    1560
ctcccgtgat cgtcacctcc aacaccaaca tgtgcgccgt gattgacggg aactcaacga    1620
ccttcgaaca ccagcagccg ttgcaagacc ggatgttcaa atttgaactc acccgccgtc    1680
tggatcatga cttttgggaag gtcaccaagc aggaagtcaa agactttttc cggtgggcaa    1740
aggatcacgt ggttgaggtg gagcatgaat tctacgtcaa aaagggtgga gccaagaaaa    1800
gacccgcccc cagtgacgca gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc    1860
agccatcgac gtcagacgcg gaagcttcga tcaactacgc agacaggtac caaaacaaat    1920
gttctcgtca cgtgggcatg aatctgatgc tgtttccctg cagacaatgc gagagaatga    1980
atcagaattc aaatatctgc ttcactcacg gacagaaaga ctgtttagag tgctttcccg    2040
tgtcagaatc tcaacccgtt tctgtcgtca aaaaggcgta tcagaaactg tgctacattc    2100
atcatatcat gggaaaggtg ccagacgctt gcactgcctg cgatctggtc aatgtggatt    2160
tggatgactg catctttgaa caataaatga tttaaatcag gtatggctgc cgatggttat    2220
cttccagatt ggctcgagga cactctctct gaaggaataa gacagtggtg gaagctcaaa    2280
cctggcccac caccaccaaa gcccgcagag cggcataagg acgacagcag gggtcttgtg    2340
cttcctgggt acaagtacct cggacccttc aacggactcg acaagggaga gccggtcaac    2400
gaggcagacg ccgcggccct cgagcacgta caaagcctac gaccggcagc tcgacagcgg    2460
agacaacccg tacctcaagt acaaccacgc cgacgcggag tttcaggagc gccttaaaga    2520
agatacgtct tttgggggca acctcggacg agcagtcttc caggcgaaaa agagggttct    2580
tgaacctctg ggcctggttg aggaacctgt taagacggct ccgggaaaaa agaggccggt    2640
agagcactct cctgtggagc cagactcctc ctcgggaacc ggaaaggcgg gccagcagcc    2700
tgcaagaaaa agattgaatt ttggtcagac tggagacgca gactcagtac ctgaccccca    2760
gcctctcgga cagccaccag cagccccctc tggtctggga actaatacga tggctacagg    2820
cagtggcgca ccaatggcag acaataacga gggcgccgac ggagtgggta attcctccgg    2880
aaattggcat tgcgattcca catggatggg cgacagagtc atcaccacca gcacccgaac    2940
ctgggccctg cccacctaca acaaccacct ctacaaacaa atttccagcc aatcaggagc    3000
ctcgaacgac aatcactact ttggctacag caccccttgg gggtattttg acttcaacag    3060
attccactgc cacttttcac cacgtgactg gcaaagactc atcaacaaca ctgggggatt    3120
ccgacccaag agactcaact tcaagctctt taacattcaa gtcaaagagg tcacgcagaa    3180
tgacggtacg acgacgattg ccaataacct taccagcacg gttcaggtgt ttactgactc    3240
ggagtaccag ctcccgtacg tcctcggctc ggcgcatcaa ggatgcctcc cgccgttccc    3300
agcagacgtc ttcatggtgc cacagtatgg atacctcacc ctgaacaacg ggagtcaggc    3360
agtaggacgc tcttcatttt actgcctgga gtactttcct tctcagatgc tgcgtaccgg    3420
aaacaacttt accttcagct cacttttga ggacgttcct ttccacagca gctacgctca     3480
cagccagagt ctggaccgtc tcatgaatcc tctcatcgac cagtacctgt attacttgag    3540
cagaacaaac actccaagtg gaaccaccac gcagtcaagg cttcagtttt ctcaggccgg    3600
agcgagtgac attcgggacc agtctaggaa ctggcttcct ggaccctgtt accgccagca    3660
gcgagtatca aagacatctg cggataacaa caacagtgaa tactcgtgga ctggagctac    3720
caagtaccac ctcaatggca gagactctct ggtgaatccg gccatggcaa gccacaagga    3780
cgatgaagaa aagttttttc ctcagagcgg ggttctcatc tttgggaagc aaggctcaga    3840
gaaaacaaat gtgaacattg aaaaggtcat gattacagac gaagaggaaa tcggaacaac    3900
caatcccgtg gctacggagc agtatggttc tgtatctacc aacctccaga gaggcaacag    3960
acaagcagct accgcagatg tcaacacaca aggcgttctt ccaggcatgg tctggcagga    4020
cagagatgtg taccttcagg ggcccatctg ggcaaagatt ccacacacgg acggacattt    4080
tcacccctct cccctcatgg gtggattcgg acttaaacac cctcctccac agattctcat    4140
caagaacacc ccggtacctg cgaatccttc gaccaccttc agtgcggcaa agtttgcttc    4200
cttcatcaca cagtactcca cgggacacgg tcagcgtgga gatcgagtgg gagctgcaga    4260
aggaaaacag caaacgctgg aatcccgaaa ttcagtacac ttccaactac aacaagtctg    4320
ttaatcgtgg acttaccgtg gatactaatg gcgtgtattc agagcctcgc cccattggca    4380
ccagatacct gactcgtaat ctgtaattgc ttgttaatca ataaaccgtt taattcgttt    4440
cagttgaact ttggtctctg cgtatttctt tcttatctag tttccatggc tacgtagata    4500
agtagcatgg cgggttaatc attaactaca aggaacccct agtgatggag ttggccactc    4560
cctctctgcg cgctcgctcg ctcactgagg ccgggcgacc aaaggtcgcc cgacgcccgg    4620
```

gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag agagggagtg gccaa   4675

<210> 25
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 25

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15
Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30
Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
            35                  40                  45
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
        50                  55                  60
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80
Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
            115                 120                 125
Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
        130                 135                 140
Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160
Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175
Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190
Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
            195                 200                 205
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
            210                 215                 220
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270
Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
            275                 280                 285
Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
        290                 295                 300
Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320
Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335
Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350
Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
            355                 360                 365
Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
370                 375                 380
```

```
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390             395                 400
Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405             410                 415
Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420             425                 430
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
            435             440                 445
Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450             455             460
Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465             470             475                 480
Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
            485             490                 495
Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500             505             510
Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
    515             520             525
Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530             535             540
Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545             550             555                 560
Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
            565             570             575
Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580             585             590
Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
    595             600             605
Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610             615             620
Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625             630             635                 640
His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
            645             650                 655
Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660             665             670
Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
    675             680             685
Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690             695             700
Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705             710             715                 720
Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
            725             730             735
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<210> 26
<211> 621
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 26
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Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1               5                   10                  15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
            20              25                  30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35              40                  45
```

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```
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
    50              55              60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65              70              75              80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
            85              90              95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100             105             110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
    115             120             125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130             135             140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145             150             155             160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
            165             170             175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
            180             185             190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
            195             200             205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210             215             220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225             230             235             240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            245             250             255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260             265             270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
            275             280             285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290             295             300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305             310             315             320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            325             330             335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340             345             350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
            355             360             365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370             375             380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385             390             395             400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            405             410             415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420             425             430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
            435             440             445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
    450             455             460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465             470             475             480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
            485             490             495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500             505             510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
            515             520             525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
```

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```
        530                     535                 540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545                     550                 555                 560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                565                 570                 575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                580                 585                 590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                595                 600                 605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
610                     615                 620
```